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RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/032,827A

DATE: 05/01/2002
TIME: 12:01:18

Input Set : A:\seqlistcorrected.txt
Output Set: N:\CRF3\05012002\J032827A.raw

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3 <110> APPLICANT: Schwartz, John J.
4      Jacobson, Joseph
5      Dasgupta, Ruchira
7 <120> TITLE OF INVENTION: Engineered Stimulus-Responsive Switches
9 <130> FILE REFERENCE: ENZ-004
11 <140> CURRENT APPLICATION NUMBER: US 10/032,827A
12 <141> CURRENT FILING DATE: 2001-10-23
14 <150> PRIOR APPLICATION NUMBER: US 60/242,546
15 <151> PRIOR FILING DATE: 2000-10-23
17 <160> NUMBER OF SEQ ID NOS: 20
19 <170> SOFTWARE: PatentIn version 3.0
21 <210> SEQ ID NO: 1
22 <211> LENGTH: 21
23 <212> TYPE: PRT
C--> 24 <213> ORGANISM: Artificial
26 <220> FEATURE:
27 <223> OTHER INFORMATION: Zinc finger consensus sequence
29 <220> FEATURE:
30 <221> NAME/KEY: misc_feature
31 <222> LOCATION: (2)..(3)
32 <223> OTHER INFORMATION: wherein Xaa at positions 2, 3 can be any amino acid
35 <220> FEATURE:
36 <221> NAME/KEY: misc_feature
37 <222> LOCATION: (5)..(7)
38 <223> OTHER INFORMATION: wherein Xaa at positions 5, 6, 7 can be any amino acid
41 <220> FEATURE:
42 <221> NAME/KEY: misc_feature
43 <222> LOCATION: (9)..(13)
44 <223> OTHER INFORMATION: wherein Xaa at positions 9, 10, 11, 12, 13 can be any amino
acid
47 <220> FEATURE:
48 <221> NAME/KEY: misc_feature
49 <222> LOCATION: (15)..(16)
50 <223> OTHER INFORMATION: wherein Xaa at positions 15, 16 can be any amino acid
53 <220> FEATURE:
54 <221> NAME/KEY: misc_feature
55 <222> LOCATION: (18)..(20)
56 <223> OTHER INFORMATION: wherein Xaa at positions 18, 19, 20 can be any amino acid
59 <400> SEQUENCE: 1
W--> 61 Cys Xaa Xaa Cys Xaa Xaa Xaa Phe Xaa Xaa Xaa Xaa Xaa Leu Xaa Xaa
62 1           5           10          15
W--> 64 His Xaa Xaa Xaa His
65           20
67 <210> SEQ ID NO: 2

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68 <211> LENGTH: 22
69 <212> TYPE: PRT
C--> 70 <213> ORGANISM: Artificial
72 <220> FEATURE:
73 <223> OTHER INFORMATION: Zinc finger consensus sequence
75 <220> FEATURE:
76 <221> NAME/KEY: misc_feature
77 <222> LOCATION: (2)..(4)
78 <223> OTHER INFORMATION: wherein Xaa at positions 2, 3, 4 can be any amino acid
81 <220> FEATURE:
82 <221> NAME/KEY: misc_feature
83 <222> LOCATION: (6)..(8)
84 <223> OTHER INFORMATION: wherein Xaa at positions 6, 7, 8 can be any amino acid
87 <220> FEATURE:
88 <221> NAME/KEY: misc_feature
89 <222> LOCATION: (10)..(14)
90 <223> OTHER INFORMATION: wherein Xaa at positions 10, 11, 12, 13, 14 can be any amino acid
acid
93 <220> FEATURE:
94 <221> NAME/KEY: misc_feature
95 <222> LOCATION: (16)..(17)
96 <223> OTHER INFORMATION: wherein Xaa at positions 16, 17 can be any amino acid
99 <220> FEATURE:
100 <221> NAME/KEY: misc_feature
101 <222> LOCATION: (19)..(21)
102 <223> OTHER INFORMATION: wherein Xaa at positions 19, 20, 21 can be any amino acid
105 <400> SEQUENCE: 2
W--> 107 Cys Xaa Xaa Xaa Cys Xaa Xaa Xaa Phe Xaa Xaa Xaa Xaa Leu Xaa
108 1 5 10 15
W--> 110 Xaa His Xaa Xaa Xaa His
111 20
113 <210> SEQ ID NO: 3
114 <211> LENGTH: 23
115 <212> TYPE: PRT
C--> 116 <213> ORGANISM: Artificial
118 <220> FEATURE:
119 <223> OTHER INFORMATION: Zinc finger consensus sequence
121 <220> FEATURE:
122 <221> NAME/KEY: misc_feature
123 <222> LOCATION: (2)..(5)
124 <223> OTHER INFORMATION: wherein Xaa at positions 2, 3, 4, 5 can be any amino acid
127 <220> FEATURE:
128 <221> NAME/KEY: misc_feature
129 <222> LOCATION: (7)..(9)
130 <223> OTHER INFORMATION: wherein Xaa at positions 7, 8, 9 can be any amino acid
133 <220> FEATURE:
134 <221> NAME/KEY: misc_feature
135 <222> LOCATION: (11)..(15)
136 <223> OTHER INFORMATION: wherein Xaa at positions 11, 12, 13, 14, 15 can be any amino acid
acid
139 <220> FEATURE:

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140 <221> NAME/KEY: misc_feature
141 <222> LOCATION: (17)..(18)
142 <223> OTHER INFORMATION: wherein Xaa at positions 17, 18 can be any amino acid
145 <220> FEATURE:
146 <221> NAME/KEY: misc_feature
147 <222> LOCATION: (20)..(22)
148 <223> OTHER INFORMATION: wherein Xaa at positions 20, 21, 22 can be any amino acid
151 <400> SEQUENCE: 3
W--> 153 Cys Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Phe Xaa Xaa Xaa Xaa Xaa Leu
154 1 5 10 15
W--> 156 Xaa Xaa His Xaa Xaa Xaa His
157 20
159 <210> SEQ ID NO: 4
160 <211> LENGTH: 21
161 <212> TYPE: PRT
C--> 162 <213> ORGANISM: Artificial
164 <220> FEATURE:
165 <223> OTHER INFORMATION: Zinc finger consensus sequence
167 <220> FEATURE:
168 <221> NAME/KEY: misc_feature
169 <222> LOCATION: (2)..(3)
170 <223> OTHER INFORMATION: wherein Xaa at positions 2, 3 can be any amino acid
173 <220> FEATURE:
174 <221> NAME/KEY: misc_feature
175 <222> LOCATION: (4)..(16)
176 <223> OTHER INFORMATION: wherein Xaa at positions 5, 6, 7, 8, 9, 10, 11, 12, 13, 14,
15, 1
177 6, 17 can be any amino aci
180 <220> FEATURE:
181 <221> NAME/KEY: misc_feature
182 <223> OTHER INFORMATION: wherein Xaa at positions 19, 20 can be any amino acid
185 <400> SEQUENCE: 4
W--> 187 Cys Xaa Xaa Cys Xaa Xaa
188 1 5 10 15
W--> 190 Xaa Cys Xaa Xaa Cys
191 20
193 <210> SEQ ID NO: 5
194 <211> LENGTH: 7
195 <212> TYPE: PRT
C--> 196 <213> ORGANISM: Artificial
198 <220> FEATURE:
199 <223> OTHER INFORMATION: target sequence for protein kinase A
201 <400> SEQUENCE: 5
203 Leu Arg Arg Ala Ser Leu Gly
204 1 5
206 <210> SEQ ID NO: 6
207 <211> LENGTH: 10
208 <212> TYPE: PRT
C--> 209 <213> ORGANISM: Artificial
211 <220> FEATURE:

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212 <223> OTHER INFORMATION: substrate for casein kinase II

214 <400> SEQUENCE: 6

216 Arg Arg Arg Glu Glu Glu Thr Glu Glu

217 1 5 10

219 <210> SEQ ID NO: 7

220 <211> LENGTH: 12

221 <212> TYPE: PRT

C--> 222 <213> ORGANISM: Artificial

224 <220> FEATURE:

225 <223> OTHER INFORMATION: substrate sequence for v-Abl tyrosine kinase

227 <400> SEQUENCE: 7

229 Glu Ala Ile Tyr Ala Ala Pro Phe Ala Lys Lys Lys

230 1 5 10

232 <210> SEQ ID NO: 8

233 <211> LENGTH: 27

234 <212> TYPE: DNA

C--> 235 <213> ORGANISM: Artificial

237 <220> FEATURE:

238 <223> OTHER INFORMATION: primer for leucine zipper motif

240 <400> SEQUENCE: 8

241 atcgcgacata tgaaacaact tgaagac

27

244 <210> SEQ ID NO: 9

245 <211> LENGTH: 22

246 <212> TYPE: DNA

C--> 247 <213> ORGANISM: Artificial

249 <220> FEATURE:

250 <223> OTHER INFORMATION: primer for leucine zipper motif

252 <400> SEQUENCE: 9

253 tcagcgttcg ccaactaatt tc

22

256 <210> SEQ ID NO: 10

257 <211> LENGTH: 26

258 <212> TYPE: DNA

C--> 259 <213> ORGANISM: Artificial

261 <220> FEATURE:

262 <223> OTHER INFORMATION: primer for lambda repressor

264 <400> SEQUENCE: 10

265 atgagcacaaa aaaagaaacc attaac

26

268 <210> SEQ ID NO: 11

269 <211> LENGTH: 18

270 <212> TYPE: DNA

C--> 271 <213> ORGANISM: Artificial

273 <220> FEATURE:

274 <223> OTHER INFORMATION: primer for lambda repressor

276 <400> SEQUENCE: 11

277 qcttacccag cgctccgc

18

280 <210> SEQ ID NO: 12

281 <211> LENGTH: 504

282 <212> TYPE: DNA

C--> 283 <213> ORGANISM: Artificial

RAW SEQUENCE LISTING
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Input Set : A:\seqlistcorrected.txt
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285 <220> FEATURE:
286 <223> OTHER INFORMATION: cI-bZIP repressor variant
288 <400> SEQUENCE: 12

289 atggagcacaa	aaaagaaaacc	attaacacaa	gagcagcttg	aggacgcacg	tcgccttaaa	60
291 qcaattttatg	aaaaaaaaagaa	aatgaactt	ggcttatccc	aggaatctgt	cgcagacaag	120
293 atggggatgg	ggcagtccgg	cgttggtgct	ttatttaatg	gcatcaatgc	attaaatgct	180
295 tataacgcgg	cattgttac	aaaaattctc	aaagtttagcq	ttgaagaatt	tagcccttca	240
297 atcgccagag	aaatctacga	gatgtatgaa	gcggtagta	tgcagccgtc	acttagaagt	300
299 gagttatgagt	accctgtttt	ttctcatgtt	caggcaggga	tgttctcacc	taagctttaga	360
301 acctttacca	aaggtgatgc	ggagcgctgg	gtaagcatcg	cgcacatgaa	acaacttgaa	420
303 gacaagggtg	aagaattgct	ttcgaaaaat	tatcaacttgg	aaaatgaggt	tgccagatta	480
305 aqaaatttag	ttggcgaacg	ctga				504

 308 <210> SEQ ID NO: 13
 309 <211> LENGTH: 35
 310 <212> TYPE: DNA
C--> 311 <213> ORGANISM: Artificial
 313 <220> FEATURE:
 314 <223> OTHER INFORMATION: primer for coding sequence of a temperature sensitive form of the

315 lambda repressor containing an Aval sit					
317 <400> SEQUENCE: 13					
318 ttacaacgcc	cgggtcagcc	aaacgtctct	tcagg		35
321 <210> SEQ ID NO: 14					
322 <211> LENGTH: 71					
323 <212> TYPE: DNA					

C--> 324 <213> ORGANISM: Artificial
 326 <220> FEATURE:
 327 <223> OTHER INFORMATION: primer for the coding sequence of a temperature sensitive form of

328 lambda represso						
330 <400> SEQUENCE: 14						
331 atgggcattt	tctcgagtca	gccggccat	accccgcatc	cggcggccag	cacaaaaaag	60
333 aaaccattaa	c					71
336 <210> SEQ ID NO: 15						
337 <211> LENGTH: 784						
338 <212> TYPE: DNA						

C--> 339 <213> ORGANISM: Artificial
 341 <220> FEATURE:
 342 <223> OTHER INFORMATION: TBD-cI chimeric repressor variant
 344 <400> SEQUENCE: 15

345 atgggcattt	tctcgagtca	gccggccat	accccgcatc	cattaacaca	agagcagcac	60
347 aaaaaagaaa	ccattaacac	aagagcagct	tgaggacgca	cgtgcctta	aagcaattt	120
349 taaaaaaaaag	aaaaatgaac	ttggcttate	ccagaatct	gtcgcagaca	agatggggat	180
351 ggggcagtca	ggcgttgtg	ctttatttaa	tggcatcaat	gcattaaatg	tttataacgc	240
353 ccattgttt	acaaaaattc	tcaaagttag	cgttgaagaa	tttagccctt	caatcgccag	300
355 aqaaatctac	gagatgtatg	aagcggttag	tatgcagccg	tcacttagaa	gtgagttatga	360
357 gtaccctgtt	catcaccatc	accatcactt	ttctcatgtt	caggcaggga	tgttctcacc	420
359 taagctttaga	acctttacca	aaggtgatgc	ggagagatgg	gtaagcacaa	ccaaaaaagc	480
361 cagtgattct	gcattctggc	ttgaggttga	aggtaattcc	atgaccgcac	caacaggctc	540
363 caagccaagc	tttcctgacg	gaatgttaat	tctcggtgac	cctgagcagg	ctgttgagcc	600
365 aqgtgatttc	tgcataagcca	gacttggggg	tgtatgagttt	accttcaaga	aactgatcag	660

RAW SEQUENCE LISTING ERROR SUMMARY
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; Xaa Pos. 2,3,5,6,7,9,10,11,12,13,15,16,18,19,20
Seq#:2; Xaa Pos. 2,3,4,6,7,8,10,11,12,13,14,16,17,19,20,21
Seq#:3; Xaa Pos. 2,3,4,5,7,8,9,11,12,13,14,15,17,18,20,21,22
Seq#:4; Xaa Pos. 2,3,5,6,7,8,9,10,11,12,13,14,15,16,17,19,20

Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:1,2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20

VERIFICATION SUMMARY

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Input Set : A:\seqlistcorrected.txt

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L:24 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:1
L:61 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:0
L:64 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:16
L:70 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:2
L:107 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:0
L:110 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:16
L:116 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:3
L:153 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:0
L:156 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:16
L:162 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:4
L:187 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:0
L:190 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:16
L:196 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:5
L:209 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:6
L:222 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:7
L:235 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:8
L:247 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:9
L:259 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:10
L:271 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:11
L:283 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:12
L:311 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:13
L:324 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:14
L:339 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:15
L:377 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:16
L:392 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:17
L:422 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:18
L:450 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:19
L:463 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:20